

Figure 1

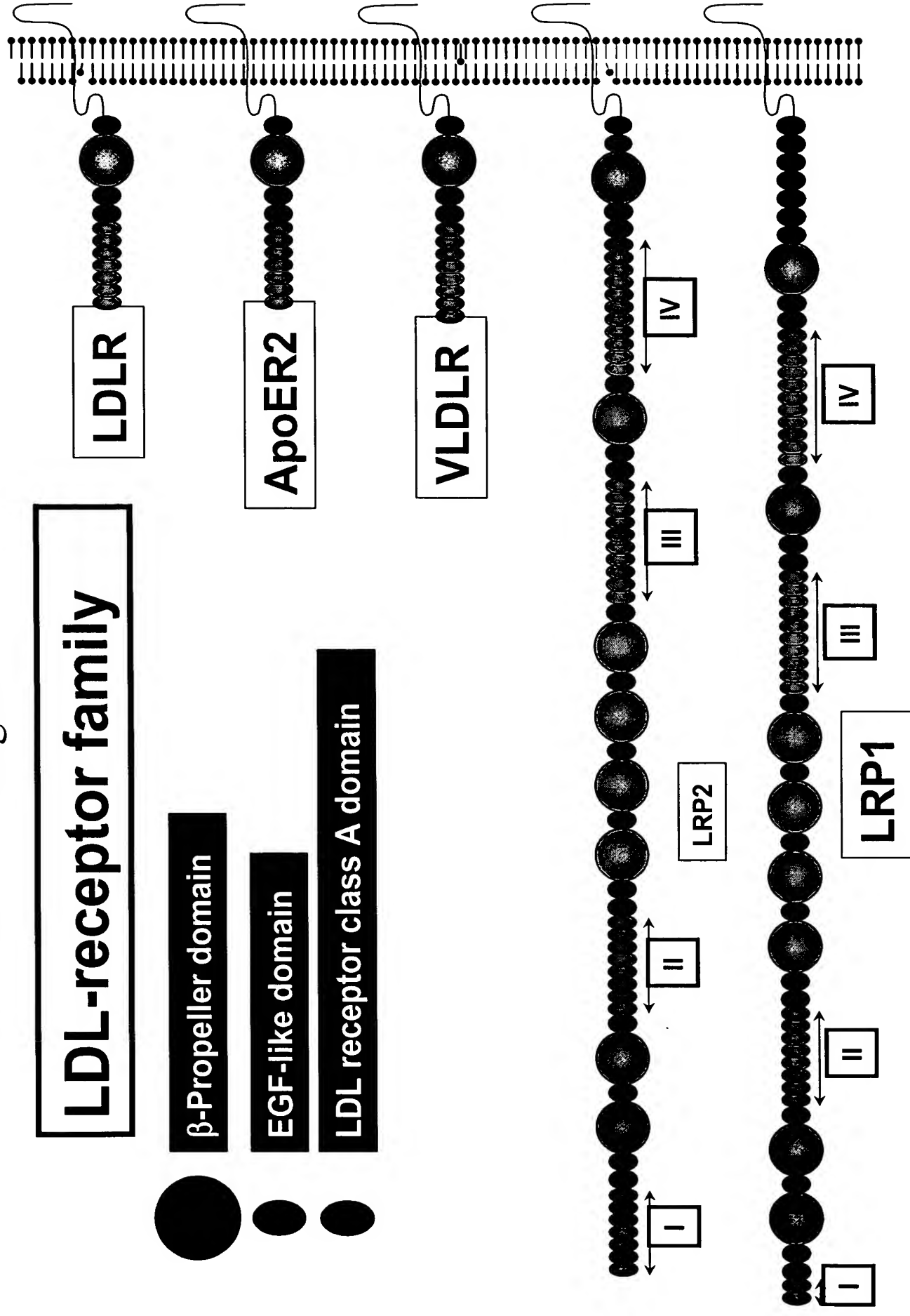


Figure 2

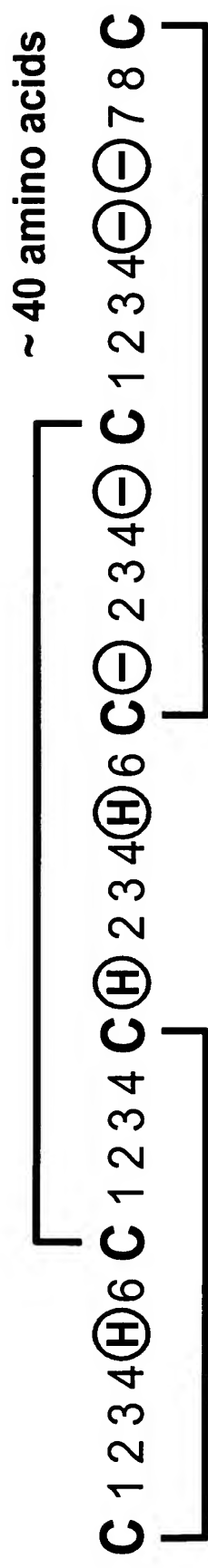
LDL-receptor class A domain

LRP1_HUMAN	C.EPYQFRCKNNR.....CVPGRWQ.CDYDNDCGDNSDEES.....C
LRP1_HUMAN	C.LPSQFKCTNTNR.....CIPGIFR.CNGQDNCGDGEDERD.....C
LDLR_HUMAN	C.SQDEFRCHDGK.....CISRQFV.CDSDRDCLDGSDEAS.....C
LRP2_HUMAN	C.SSSAFTCGHGE.....CIPAHWR.CDKRND CVDGSDEHN.....C
LRP2_HUMAN	C.SSSEFQCASGR.....CIPQHWY.CDQETDCFDASDEPAS.....C
CORI_HUMAN	CHSQGLVECRNGQ.....CIPSTFQ.CDGDEDCCKDGSDEEN.....C
MAT_HUMAN	C.PAQTFRC SNGK.....CLSKSQQ.CNGKDDCGDGSDEAS.....C
CO8B_HUMAN	C...EGFVCAQTGR.....CVNRRLL.CNGDND CGDQSDEAN.....C
MAT_HUMAN	C.TKHTYRCLNGL.....CLSKGNPECDGKEDCSDGSDEKD.....C
LDVR_HUMAN	CLGPGKFKCRSGE.....CIDISKV.CNQEQDCRDWSDEPLKE..C
APOER2_HUM	C.PAEKLSCGPTSHK...CVPASWR.CDGEKDCEGGADEAG.....C
SORL_HUMAN	CTHFMDFVCKNRQQ.....CLFHSMV.CDGIIQCRDGSDEDAAFAGC
ST7_HUMAN	C.AYNQFQCLSRFTKVYTCLPESLK.CDGNIDCLDLGDEID.....C
consensus	<div> <div>C.1234F6C12G4.....CI23456.CDG34DC1D3SDE78.....C</div> <div> <div></div> <div>*</div> <div>*</div> <div>*</div> <div>*</div> </div> </div>

FIGURE 3

A-domains

A



B

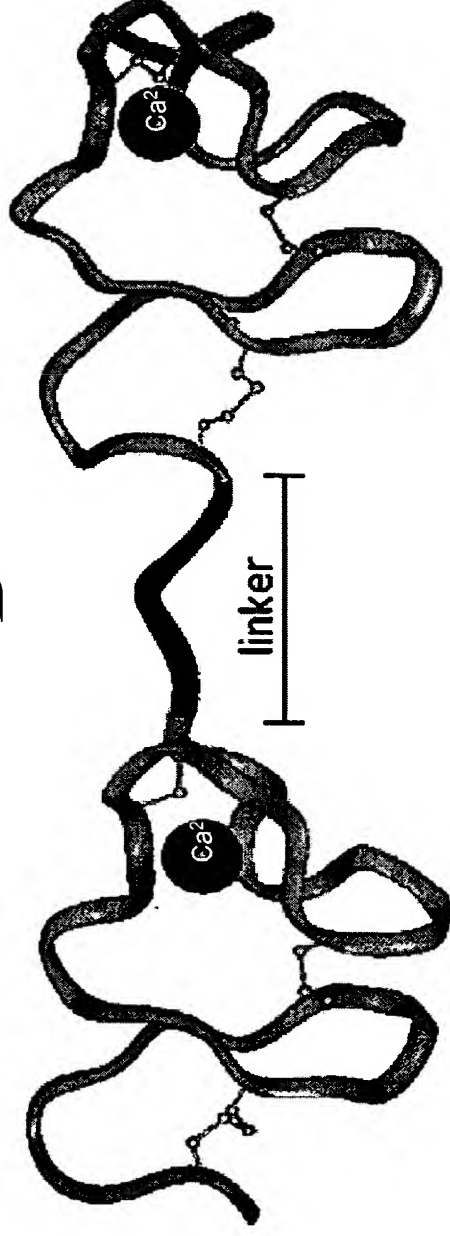


Figure 4

Ligands recognized by LDL-receptor family

proteases	proteins involved in	miscellaneous
factor IXa	lipoprotein metabolism	albumin
pro-uPA	apoB100	transthyretin
t-PA	apoE	β -Amyloid precursor protein
plasminogen	apoJ (clusterin)	RAP
MMP-9	apoH (β_2 -glycoprotein I)	complement C3
	Lp(a)	lactoferrin
inhibitors	hepatic lipase	thyroglobulin
α_2 -macroglobulin	lipoprotein lipase	thrombospondin
PAI-1	IDL	saposin precursor
TFPI	VLDL	reelin
pancreatic trypsin inhibitor	β -VLDL	insulin
		parathyroid hormone (PTH)
complexes	non-human	aprotinin
protease/	pseudomonas exotoxin A	α -amylase
α_1 -antitrypsin	circumsporozoite protein	C1q
protein C inhibitor	trichosanthin	α_1 -microglobulin
protease nexin-1	ricin A	β_2 -microglobulin
antithrombin	saporin	odorant-binding protein
C1-inhibitor	antibiotics	epidermal growth factor
thrombin/heparin cofactor II	gentamicin	prolactin
cathepsin G/ α_1 -antichymotrypsin	polymyxin B	lysozyme
vitamin-carrier complexes	viruses	connective tissue growth factor (CTGF)
vitamin D-bp, vitamin D	HRV2 (Rhino)	cytochrome c
retinol-bp, vitamin A	HCV (Flavi)	seminal vesicle secretory protein II
transcobalamin, vitamin B12	BVDV (Flavi)	clara cell secretory protein (CCSP)
		cubulin
		factor VIII

Figure 5

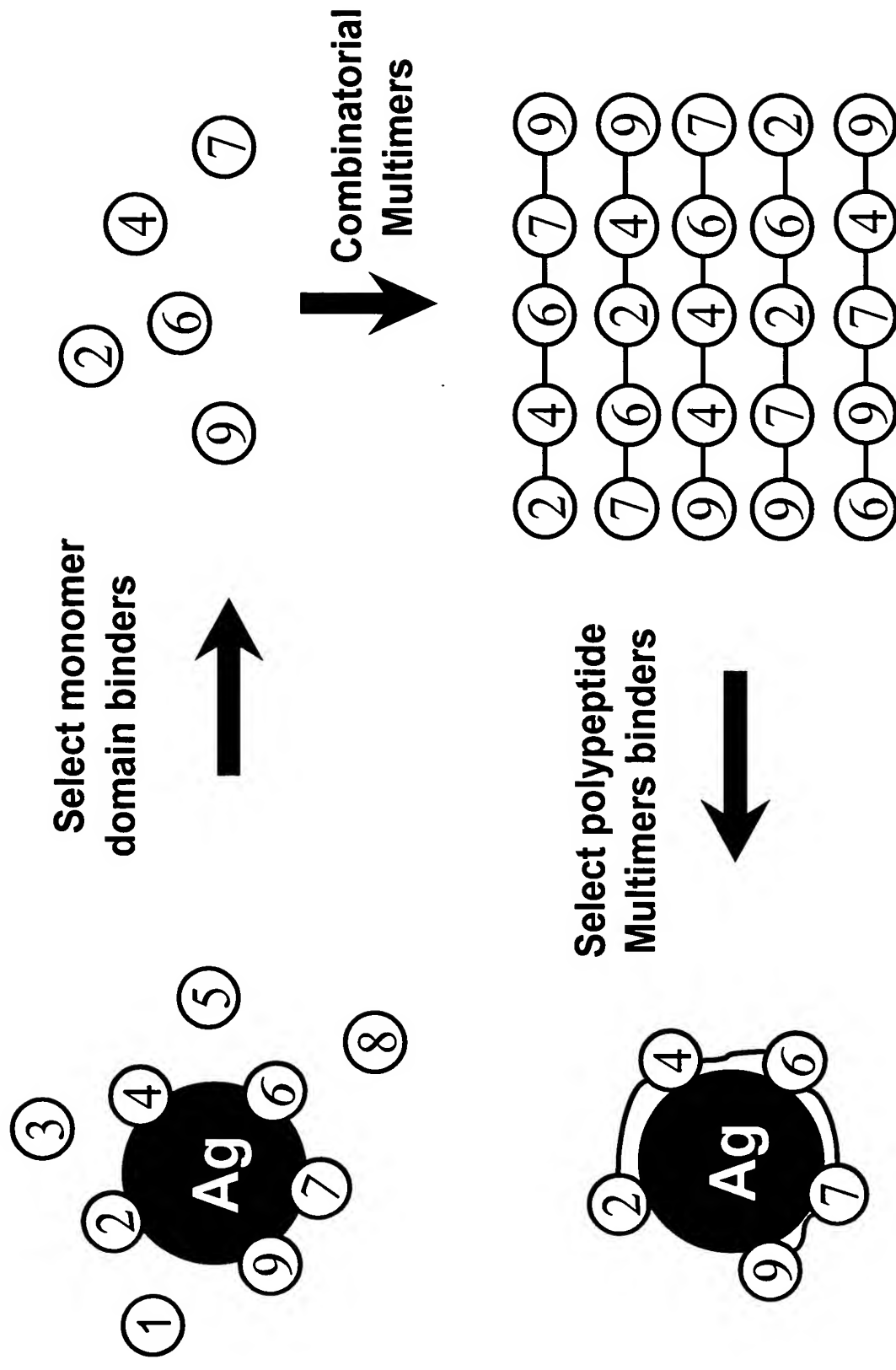


Figure 6

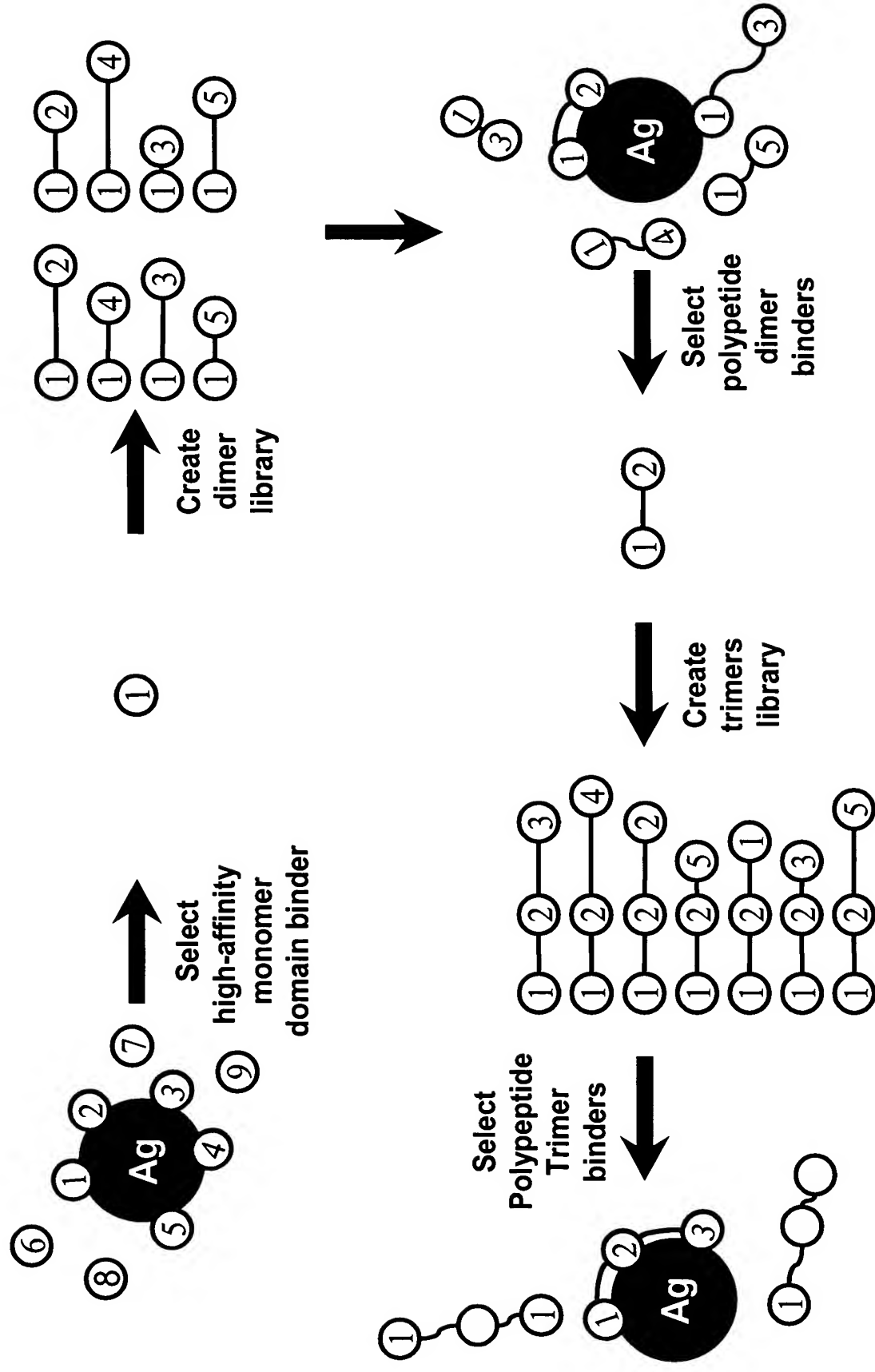


Figure 7

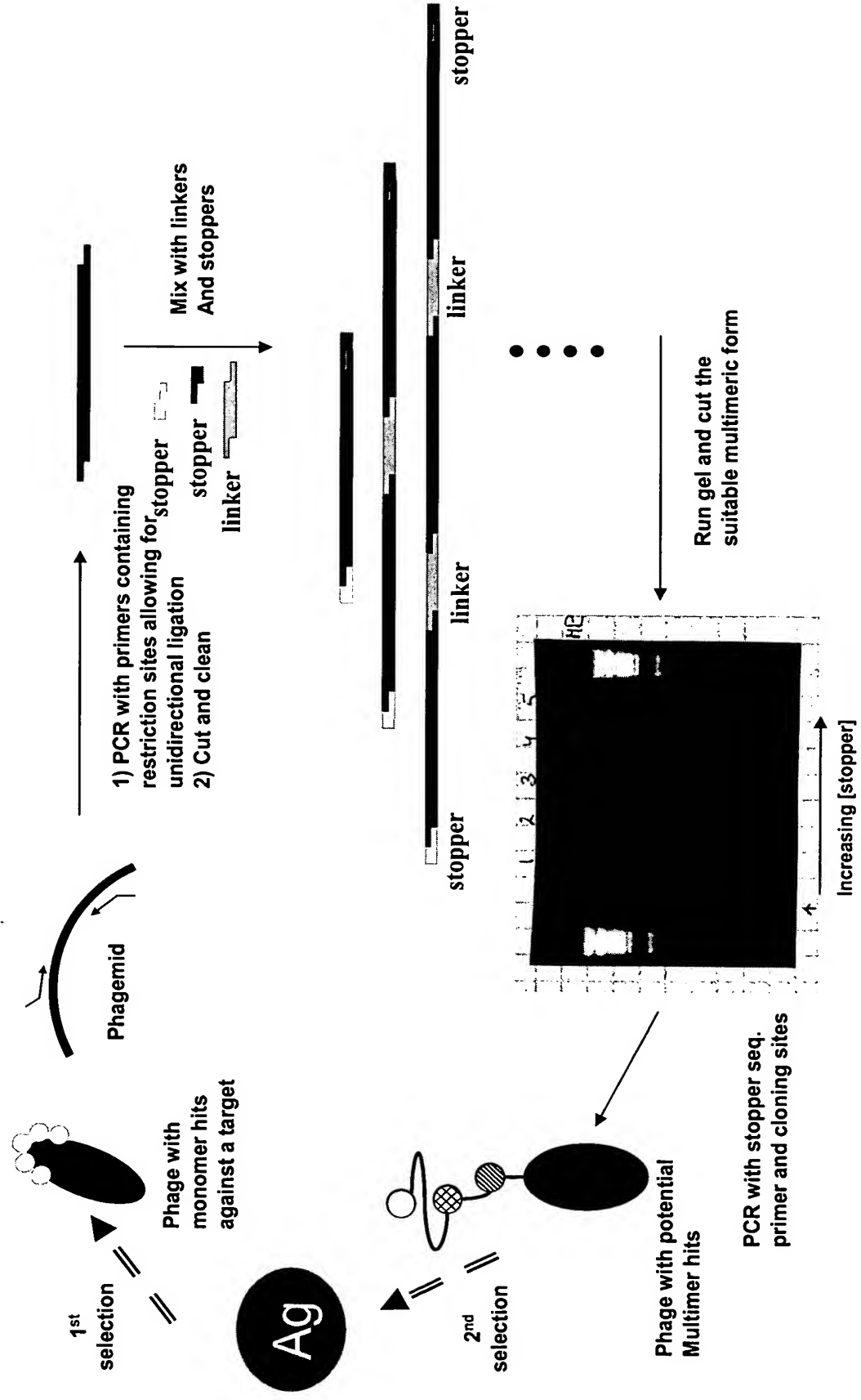


Figure 8

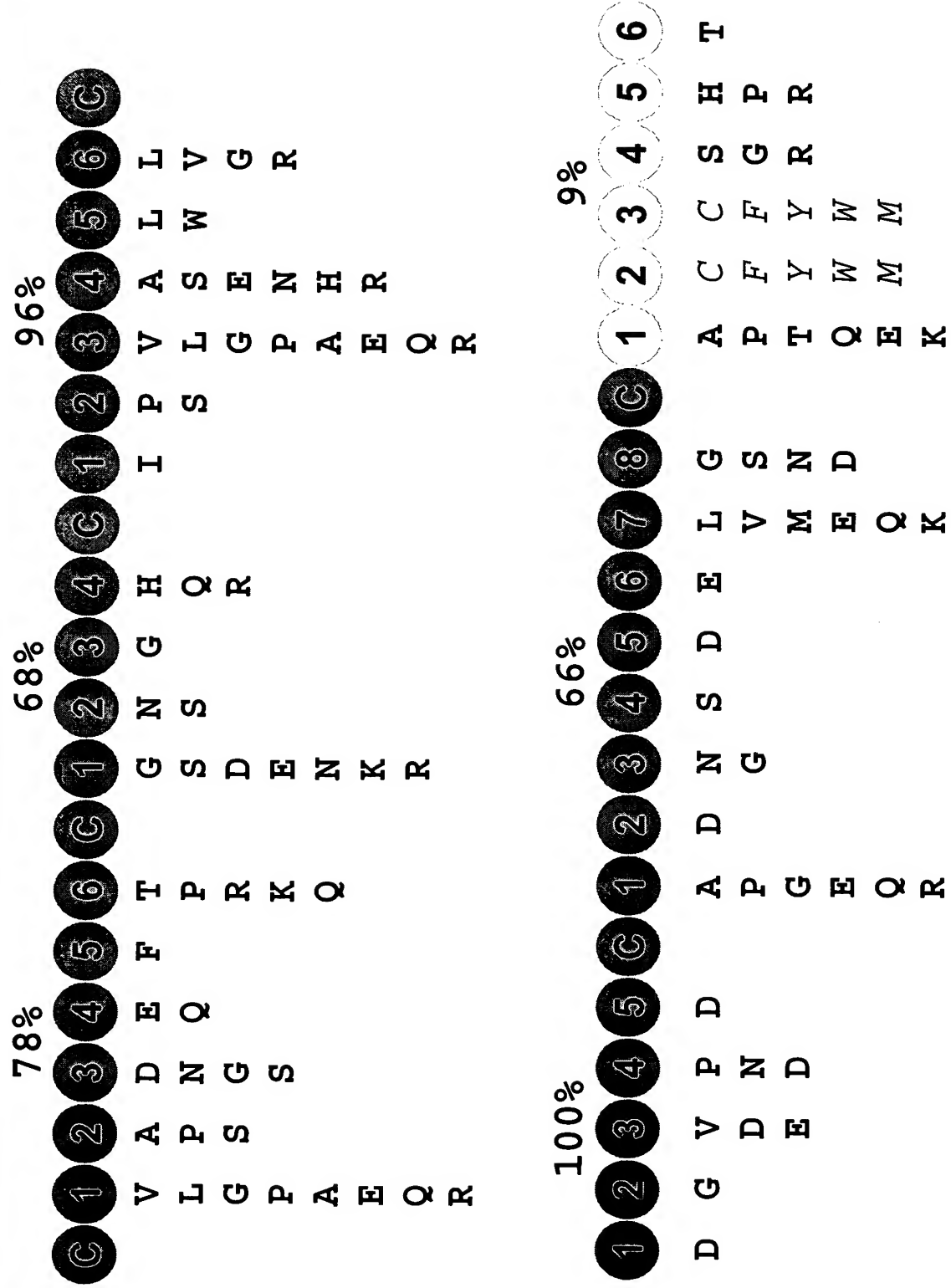


FIG. 9A

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
A	0.0	<u>7.1</u>	12.3	3.2	1.9	1.9	7.1	0.0	15.8	1.5	0.0	1.5	0.0	1.0	3.7	7.3	9.4
C	100.0	0.0	0.6	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	1.5	99.5	0.0	0.0	0.0	0.0
D	0.0	5.2	4.5	19.5	2.6	0.0	0.0	0.0	8.3	<u>10.5</u>	2.3	0.8	0.0	0.0	3.7	1.6	4.7
E	0.0	4.5	9.7	2.6	37.0	0.0	3.9	0.0	3.8	0.0	0.8	9.8	0.0	0.0	1.6	7.3	7.3
F	0.0	0.6	0.0	3.9	1.9	76.0	0.6	0.0	0.8	0.0	0.0	0.8	0.0	0.5	1.6	2.1	2.6
G	0.0	13.0	3.2	16.2	1.9	0.0	0.0	0.0	12.8	0.8	72.2	2.3	0.0	0.0	3.1	<u>5.2</u>	4.2
H	0.0	1.9	1.3	<u>5.2</u>	3.9	1.9	3.9	0.0	3.0	0.8	4.5	9.0	0.0	0.0	4.7	3.1	5.8
I	0.0	0.0	1.3	0.0	0.0	3.9	0.6	0.0	0.0	0.0	0.0	2.3	0.0	63.9	0.0	<u>5.2</u>	3.7
K	0.0	3.9	3.9	1.9	1.9	0.6	<u>7.8</u>	0.0	11.3	0.0	3.0	<u>9.0</u>	0.0	2.1	2.1	<u>9.9</u>	3.7
L	0.0	8.4	4.5	0.0	1.3	3.9	3.9	0.0	1.5	0.0	1.5	4.5	0.0	<u>11.0</u>	<u>5.2</u>	12.0	3.1
M	0.0	0.6	0.6	0.0	1.3	0.6	1.9	0.0	0.0	0.0	0.0	0.8	0.0	0.0	<u>0.5</u>	3.1	1.6
N	0.0	1.9	0.6	13.6	1.3	0.0	1.9	0.0	<u>5.3</u>	51.9	<u>5.3</u>	3.8	0.0	0.0	<u>5.2</u>	4.2	2.6
P	0.0	10.4	33.8	1.3	0.0	0.0	9.7	0.0	4.5	0.0	0.0	0.0	0.0	0.0	45.5	7.3	2.1
Q	0.0	10.4	2.6	1.9	30.5	0.6	21.4	0.0	5.3	0.8	2.3	9.8	0.0	0.0	2.6	5.8	4.7
R	0.0	7.1	3.2	3.2	1.3	0.6	18.2	0.0	<u>7.5</u>	0.8	4.5	32.3	0.0	0.0	1.0	<u>9.4</u>	11.5
S	0.0	18.8	11.7	16.2	3.9	0.6	9.7	0.0	<u>15.0</u>	25.6	3.0	3.0	0.0	0.0	14.7	<u>10.5</u>	20.4
T	0.0	<u>5.2</u>	2.6	<u>5.8</u>	3.2	1.3	<u>7.8</u>	0.0	2.3	<u>6.0</u>	0.8	<u>6.0</u>	0.0	1.6	2.6	0.5	<u>5.8</u>
V	0.0	0.6	1.9	0.6	0.0	0.6	1.3	0.0	2.3	0.8	0.0	3.0	0.0	<u>17.3</u>	0.5	3.1	2.6
W	0.0	0.0	0.6	1.9	0.0	1.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	2.6
Y	0.0	0.0	0.6	2.6	<u>5.8</u>	5.2	0.0	0.0	0.8	0.8	0.0	0.0	0.5	2.6	1.0	2.1	1.6
	100.0	85.7	67.5	76.6	73.4	81.2	81.8	100.0	81.2	94.0	77.4	75.9	99.5	92.1	70.7	80.1	60.2
1	9	4	6	3	2	2	7	1	8	4	2	6	1	3	4	10	6
100.0	73.4	67.5	65.6	67.5	76.0	76.0	66.2	100.0	68.4	77.4	72.2	60.9	99.5	63.9	60.2	60.2	59.2
1	7	4	4	4	2	1	5	1	6	2	1	4	1	1	2	7	6

FIG. 9B

18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
1.6	2.6	0.0	0.0	1.0	2.5	<u>5.6</u>	0.0	0.0	<u>6.9</u>	0.0	4.6	4.6	0.0	0.0	16.0	3.8	0.0
0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
1.0	0.0	0.0	81.2	1.5	28.4	22.3	86.3	0.0	3.8	89.3	1.5	0.0	100.0	0.0	<u>6.9</u>	21.4	0.0
1.0	1.6	0.0	0.0	2.0	15.7	<u>4.6</u>	3.6	0.0	9.9	0.0	2.3	6.9	0.0	100.0	<u>16.8</u>	0.8	0.0
<u>7.9</u>	0.5	0.0	0.0	0.5	4.6	3.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	1.5	0.8	0.0
1.0	0.0	0.0	0.0	66.0	0.5	0.0	0.0	0.0	30.5	1.5	48.9	1.5	0.0	0.0	0.8	22.9	0.0
0.0	2.6	0.0	0.0	3.6	4.1	1.5	3.6	0.0	0.8	0.8	2.3	0.0	0.0	0.0	2.3	6.1	0.0
0.0	4.7	0.0	0.0	0.0	4.6	2.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	3.1	0.8	0.0
<u>6.8</u>	<u>12.6</u>	0.0	0.0	1.0	2.5	<u>5.1</u>	0.0	0.0	6.1	0.0	3.8	0.0	0.0	0.0	12.2	0.8	0.0
<u>14.7</u>	15.2	0.0	0.0	1.5	2.0	3.0	0.0	0.0	<u>6.9</u>	0.0	1.5	0.8	0.0	0.0	9.9	0.8	0.0
0.5	1.0	0.0	0.0	1.5	1.0	0.0	0.0	0.0	1.5	0.0	3.1	0.8	0.0	0.0	1.5	0.8	0.0
2.1	0.0	0.0	18.8	3.6	2.0	21.3	4.1	0.0	0.0	4.6	14.5	0.0	0.0	0.0	1.5	33.6	0.0
0.0	0.5	0.0	0.0	0.0	0.0	10.7	0.0	0.0	9.9	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0
<u>5.8</u>	<u>7.3</u>	0.0	0.0	4.1	10.7	4.6	1.5	0.0	<u>5.3</u>	0.8	3.1	0.0	0.0	0.0	6.1	0.8	0.0
<u>3.7</u>	24.1	0.0	0.0	5.6	2.5	6.1	0.0	0.0	3.8	0.0	2.3	3.1	0.0	0.0	<u>10.7</u>	1.5	0.0
1.0	0.0	0.0	0.0	3.0	2.0	2.0	0.5	0.0	7.6	1.5	4.6	80.9	0.0	0.0	0.8	4.6	0.0
0.5	2.6	0.0	0.0	2.5	1.5	2.0	0.5	0.0	0.8	0.8	0.0	1.5	0.0	0.0	2.3	0.0	0.0
1.0	21.5	0.0	0.0	0.5	10.2	3.6	0.0	0.0	4.6	0.0	0.0	0.0	0.0	0.0	<u>6.1</u>	0.0	0.0
46.6	2.6	0.0	0.0	0.5	2.0	1.5	0.0	0.0	0.0	0.0	3.1	0.0	0.0	0.0	0.8	0.0	0.0
4.7	0.5	0.0	0.0	1.5	3.0	1.0	0.0	0.0	0.0	0.8	3.8	0.0	0.0	0.0	0.8	0.0	0.0
81.7	80.6	100.0	100.0	71.6	65.0	71.1	86.3	100.0	83.2	89.3	63.4	87.8	100.0	100.0	84.7	84.0	100.0
5	5	1	2	2	4	6	1	1	8	1	2	2	1	1	8	4	1
61.3	60.7	100.0	81.2	66.0	65.0	60.4	86.3	100.0	64.1	89.3	63.4	80.9	100.0	100.0	61.1	77.9	100.0
2	3	1	1	1	4	4	1	1	5	1	2	1	1	1	5	3	1

Figure 10

	a	b c	de	f	ghi	jk	lm	nop	q
IDD_HUMAN	C.....	NPGQFACRSGTIQ.....	CIPLPWQ.CDGWATCEDE.....	SDEAN.....	C				
LRP3_HUMAN	C.....	QADEFRCDNGK.....	CLPGPWQ.CNTVDECGDG.....	SDEGN.....	C				
LRP3_HUMAN	C.....	PGGTFFPCSGARSTR.....	CLPVERR.CDGLQDCGDG.....	SDEAG.....	C				
LRP3_HUMAN	C.....	LPWEQPCGSSSDSDGGS LGDQGC	CFSEPQR.CDGWWHCASG.....	RDEQG.....	C				
LRP3_HUMAN	C.....	PPDQYPCEGGSGL.....	CYTPADR.CNNQKSCPDG.....	ADEKN.....	C				
LRP3_HUMAN	C.....	QPGTFHCGTNL.....	CIFETWR.CDQEDCQDG.....	SDEHG.....	C				
LRP5_HUMAN	C.....	SPDQFACATGEID.....	CIPGAWR.CDGFPECDDQ.....	SDEEG.....	C				
LRP5_HUMAN	C.....	SAAQFPCARGQ.....	CVDLRLR.CDGEADCQDR.....	SDEVD.....	C				
LRP5_HUMAN	C.....	LPNQFRCASGQ.....	CVLIKQK.CDSFPDCIDG.....	SDELM.....	C				
LRP6_HUMAN	C.....	SPQOFTCFTGEID.....	CIPVAWR.CDGFTECEDH.....	SDELN.....	C				
LRP6_HUMAN	C.....	SESQFQCASGQ.....	CIDGALR.CNGDANCQDK.....	SDEKN.....	C				
LRP6_HUMAN	C.....	LIDQFRCANGQ.....	CIGKHKK.CDHNVD CSDK.....	SDELD.....	C				
ST7_HUMAN	C.....	ACDQFRCGNGK.....	CIPPAWK.CNNMDECGDS.....	SDEEI.....	C				
ST7_HUMAN	C.....	AYNQFQCLSRFTKVYT.....	CLPESLK.CDGNIDCLDL.....	GDEID.....	C				
ST7_HUMAN	C.....	LPWEIPCGGNWG.....	CYTEQQR.CDGYWHCPNG.....	RDETN.....	C				
ST7_HUMAN	C.....	QKEEFPCSRNGV.....	CYPRSDR.CNYQNHCPNG.....	SDEKN.....	C				
ST7_HUMAN	C.....	QPGNFHCKNNR.....	CVFESWV.CDSQDDCGDG.....	SDEEN.....	C				
CORI_HUMAN	C.....	GRGENFLCASGI.....	CIPGKLQ.CNGYND CDDW.....	SDEAH.....	C				
CORI_HUMAN	C.....	SENLFHCHTGK.....	CLNYSLV.CDGYDDCGDL.....	SDEQN.....	C				
CORI_HUMAN	C.....	NPTTEHRCGDGR.....	CIAMEWV.CDGDHDCVDK.....	SDEVN.....	C				
CORI_HUMAN	C.....	HSQGLVECRNGQ.....	CIPSTFQ.CDGEDCKDG.....	SDEEN.....	C				
CORI_HUMAN	C.....	SPSHFKCRSGQ.....	CVLASRR.CDQADCDDD.....	SDEEN.....	C				
CORI_HUMAN	C.....	KERDLWECPSNKQ.....	CLKHTVI.CDGFPCPDY.....	MDEKN.....	C				
CORI_HUMAN	C.....	QDDELECANHA.....	CVSRDLW.CDGEADCSDS.....	SDEWD.....	C				
TMS2_HUMAN	C.....	SNSGIECDSSGT.....	CINPSNW.CDGVSHCPGG.....	EDENR.....	C				
TMS3_HUMAN	C.....	SGKYRCRSSFK.....	CIELIAR.CDGVSDCKDG.....	EDEYR.....	C				
MAT_HUMAN	C.....	PGQFTCRTGR.....	CIRKELR.CDGWADCTDH.....	SDELN.....	C				
MAT_HUMAN	C.....	DAGHQFTCKNKF.....	CKPLFWV.CDSVND CGDN.....	SDEQG.....	C				
MAT_HUMAN	C.....	PAQTFRCSSNGK.....	CLSKSQQ.CNGKDDCGDG.....	SDEAS.....	C				
MAT_HUMAN	C.....	TKHTYRCLNGL.....	CLSKGNPEC DGKEDCS DG.....	SDEKD.....	C				
ENTK_HUMAN	C.....	LPGSSPCTDALT.....	CIKADLF.CDGEVNC PDG.....	SDEDNKM.....	C				
ENTK_HUMAN	C.....	KADHFQCKNGE.....	CVPLVNL.CDGLHLCEDG.....	SDEAD.....	C				
HAI1_HUMAN	C.....	QPTQFRCSSNGC.....	CIDSFLE.CDDTPNCPDA.....	SDEAA.....	C				
CFAI_HUMAN	C.....	YTQKADSPMDDFFQCVNGK.....	YISQMKK.CDGINDCGDQ.....	SDEL.....	C				
CFAI_HUMAN	C.....	QKGKFHCKSGV.....	CIPSQYQ.CNGEVDCITG.....	EDEVG.....	C				
CO6_HUMAN	C.....	KNKFRCDSGR.....	CIARKLE.CNGENDCGDN.....	SDERD.....	C				
CO7_HUMAN	C.....	GERFRCFSGQ.....	CISKSLV.CNGSDDCEDS.....	ADEDR.....	C				
CO8A_HUMAN	C.....	GQDFQCKETGR.....	CLKRHLV.CNGDQDCLDG.....	SDEDD.....	C				
CO8B_HUMAN	C.....	EGFVCAQTGR.....	CVNRRLL.CNGDNDCGDQ.....	SDEAN.....	C				
CO9_HUMAN	C.....	GNDFQCSTGR.....	CIKMRLR.CNGDNDCGDF.....	SDEDD.....	C				
PERL_HUMAN	C.....	TEAEFACHSYNE.....	CVALEYR.CDRRPDCRDM.....	SDELN.....	C				
PERL_HUMAN	C.....	GPQEAACRNGH.....	CIPRDYL.CDQEDCEDG.....	SDELD.....	C				
PERL_HUMAN	C.....	EPNEFFPCGNH.....	CALKLWR.CDGD FDCEDR.....	TDEAN.....	C				
PERL_HUMAN	C.....	GPTQFRCVSTNM.....	CIPASFH.CDEESDCPDR.....	SDEFG.....	C				
SORL_HUMAN	C.....	LRNQYRCSSNG.....	CINSIWW.CDFDND CGDM.....	SDERN.....	C				
SORL_HUMAN	C.....	DLDTQFRCQESGT.....	CIPLSYK.CDLEDDCGDN.....	SDESH.....	C				
SORL_HUMAN	C.....	RSDEYNCSSEGM.....	CIRSSWV.CDGDND CRDW.....	SDEAN.....	C				
SORL_HUMAN	C.....	EASNFQCRNGH.....	CIPQRWA.CDGD TDCQDG.....	SDEDPVN.....	C				
SORL_HUMAN	C.....	NGFRCPNGT.....	CIPSSKH.CDGLRDCSDG.....	SDEQH.....	C				
SORL_HUMAN	C.....	THFMD FVCKNRQQ.....	CLFHSMV.CDGIIQCRDG.....	SDDEAAFAG.....	C				
SORL_HUMAN	C.....	DEFGFQCQNGV.....	CISLIWK.CDGMDDCGDY.....	SDEAN.....	C				
SORL_HUMAN	C.....	SRYFQFRCENGH.....	CIPNRWK.CDREND CGDW.....	SDEKD.....	C				
SORL_HUMAN	C.....	LPNYYRCSSGT.....	CVMDTWV.CDGYRDCADG.....	SDEEA.....	C				
SORL_HUMAN	C.....	DRFEFECHQPKT.....	CIPNWKR.CDGHQDCQDG.....	RDEAN.....	C				
SORL_HUMAN	C.....	MSREFQCEDGEA.....	CIVLSER.CDGFLDCSDE.....	SDEKA.....	C				
APOER2_HUM	C.....	EKDQFQCRNER.....	CIPSVWR.CDEDDDCLDH.....	SDEDD.....	C				
APOER2_HUM	C.....	ASDFTCDNGH.....	CIHERWK.CDGEEECPDG.....	SDESEAT.....	C				
APOER2_HUM	C.....	PAEKLSCGPTSHK.....	CVPASWR.CDGEKDCEGG.....	ADEAG.....	C				
APOER2_HUM	C.....	APHEFQCNGRS.....	CLAAV FV.CDGD DDCGDG.....	SDERG.....	C				
APOER2_HUM	C.....	GPREFRCGGDGGGA.....	CIPERWV.CDRQFDCEDR.....	SDEAAEL.....	C				
APOER2_HUM	C.....	ATVSQFACRSGE.....	CVHLGWR.CDGD RDCDK.....	SDEAD.....	C				
APOER2_HUM	C.....	RGDEFQCGDGT.....	CVLAIKH.CNQEQDCPDG.....	SDEAG.....	C				
LDLR_HUMAN	C.....	ERNEFQCGDGK.....	CISYK WV.CDGS AECQDG.....	SDSQET.....	C				
LDLR_HUMAN	C.....	KSGDFSCGGRVNR.....	CIPQFWR.CDGVVDCDNG.....	SDEQG.....	C				
LDLR_HUMAN	C.....	SQDEFRC HDGK.....	CISRQFV.CDSDRDCLDG.....	SDEAS.....	C				
LDLR_HUMAN	C.....	GPASFQCNSSST.....	CIPQLWA.CDNPDPCEDG.....	SDEWQR.....	C				
LDLR_HUMAN	C.....	SAFEFHCLSGE.....	CIHSSWR.CDGGPDCKDK.....	SDEEN.....	C				
LDLR_HUMAN	C.....	RPDEFQCS DGN.....	CIHGS RQ.CDREYDCDKM.....	SDEVG.....	C				
LDLR_HUMAN	C.....	EGPNKFKCHSGE.....	CITLDKV.CNMARDCRDW.....	SDEPIKE.....	C				

LDVR_HUMAN	C.....	EPSQFQCTNGR.....	CITLLWK	CDGDEDCVDG.....	SDEKN.....	C
LDVR_HUMAN	C.....	AESDFVCNNGQ.....	CVPSRWK	CDGDPDCEDG.....	SDESPEQ.....	C
LDVR_HUMAN	C.....	RIHEISCGAHSTQ.....	CIPVSWR	CDGENDCDSDG.....	EDEEN.....	C
LDVR_HUMAN	C.....	SPDEFTCSSGR.....	CISRNFV	CNGQDDCSDG.....	SDELD.....	C
LDVR_HUMAN	C.....	GAHEFQCSTSS.....	CIPISWV	CDDADDCSDQ.....	SDESLEQ.....	C
LDVR_HUMAN	C.....	PASEIQCGSGE.....	CIHKKWR	CDGDPDCKDG.....	SDEVN.....	C
LDVR_HUMAN	C.....	RPDQFECEDGS.....	CIHGSRQ	CNGIRDCVDG.....	SDEVN.....	C
LDVR_HUMAN	C.....	LGPQKFKCRSGE.....	CIDISKV	CNQEQDCRDW.....	SDEPLKE.....	C
LRP1_HUMAN	C.....	SPKQFACRDQIT.....	CISKGWR	CDGERDCPDG.....	SDEAPEI.....	C
LRP1_HUMAN	C.....	QPNEHNCGLTEL.....	CVPMSSL	CNGVQDCMDG.....	SDEGPH.....	C
LRP1_HUMAN	C.....	QPGEFACANSR.....	CIQERWK	CDGDNDCLDN.....	SDEAPAL.....	C
LRP1_HUMAN	C.....	PSDRFKCENNR.....	CIPNRWL	CDGDNDCGNS.....	EDESNAT.....	C
LRP1_HUMAN	C.....	PPNQFSCASGR.....	CIPISWT	CDLDDDCGDR.....	SDESAS.....	C
LRP1_HUMAN	C.....	FPLTQFTCNNGR.....	CININWR	CDNDNDCGDN.....	SDEAG.....	C
LRP1_HUMAN	C.....	SSTQFKCNSGR.....	CIPHEWT	CDGDNDCGDY.....	SDETHAN.....	C
LRP1_HUMAN	C.....	HTDEFQCRDLGL.....	CIPLRWR	CDGDTDCMDS.....	SDEKS.....	C
LRP1_HUMAN	C.....	DPSVKFGCKDSAR.....	CISKAWV	CDGDNDCEDN.....	SDEEN.....	C
LRP1_HUMAN	C.....	RPPSHPCANNTSV.....	CLPPDKL	CDGNDDCGDG.....	SDEGEL.....	C
LRP1_HUMAN	C.....	RAQDEFECANGE.....	CINFSLT	CDGVPHCKDK.....	SDEKPSY.....	C
LRP1_HUMAN	C.....	KKTFRQCSNGR.....	CVSNMLW	CNGADDCGDG.....	SDEIP.....	C
LRP1_HUMAN	C.....	GVGEFRCDGT.....	CIGNSSR	CNQFVDCEDA.....	SDEMNI.....	C
LRP1_HUMAN	CSSYFRLGVKGVLFQPCERTSL.....		CYAPSWV	CDGANDCGDY.....	SDERD.....	C
LRP1_HUMAN	C.....	PLNYFACPSGR.....	CIPMSWT	CDKEDDCHEG.....	EDETH.....	C
LRP1_HUMAN	C.....	SEAQFECQNRH.....	CISKQWL	CDGSDDCGDG.....	SDEAAH.....	C
LRP1_HUMAN	C.....	GPSSFSCPGTHV.....	CVPERWL	CDGDKDCADG.....	ADESIAAG.....	C
LRP1_HUMAN	C.....	DDREFMCONRQ.....	CIPKHV	CDHHRDCADG.....	SDESPE.....	C
LRP1_HUMAN	C.....	GPSEFRCANR.....	CLSSRQWE	CDGENDCHDQ.....	SDEAPKNPH.....	C
LRP1_HUMAN	C.....	NASSQFLCSSGR.....	CVAEALL	CNGQDDCGDS.....	SDEGR.....	C
LRP1_HUMAN	C.....	TASQFVCKNDK.....	CIPFWWK	CDTEDDCGDH.....	SDEPPD.....	C
LRP1_HUMAN	C.....	RPQFQCSGTI.....	CTNPAFI	CDGDNDCCDN.....	SDEAN.....	C
LRP1_HUMAN	C.....	LPSQFKCTNTNR.....	CIPGIFR	CNGQDNCGDG.....	EDERD.....	C
LRP1_HUMAN	C.....	APNQFQCSITKR.....	CIPRVVW	CDRDNDCCVDG.....	SDEPAN.....	C
LRP1_HUMAN	C.....	GVDEFRCDSGR.....	CIPARWK	CDGEDDCGDG.....	SDEPKEE.....	C
LRP1_HUMAN	C.....	EPYQFRCKNNR.....	CVPGRWQ	CDYDNDCCDN.....	SDEES.....	C
LRP1_HUMAN	C.....	SESEFSCANR.....	CIAGRWK	CDGDHDCADG.....	SDEKD.....	C
LRP1_HUMAN	C.....	DMDQFQCKSGH.....	CIPLRWR	CDADADCMDG.....	SDEEA.....	C
LRP1_HUMAN	C.....	PLDEFQCNNTL.....	CKPLAWK	CDGEDDCGDN.....	SDENPEE.....	C
LRP1_HUMAN	C.....	PPNRPFRCKNDRV.....	CLWIGRQ	CDGTDNCGDG.....	TDEED.....	C
LRP1_HUMAN	C.....	KDKKEFLCRNQR.....	CLSSSLR	CNMFDDCGDG.....	SDEED.....	C
LRP2_HUMAN	C.....	DSAHFRCGSGH.....	CIPADWR	CDGDKDCSDG.....	ADEIG.....	C
LRP2_HUMAN	C.....	QQGYFKCQSEGQ.....	CIPSSWV	CDQDQDCDDG.....	SDERQD.....	C
LRP2_HUMAN	C.....	SSHQITCSNGQ.....	CIPSEYR	CDHVRDCPDG.....	ADEND.....	C
LRP2_HUMAN	C.....	EQLTCDNGA.....	CYNTSQK	CDWKVDCRDS.....	SDEIN.....	C
LRP2_HUMAN	C.....	LHNEFSCNGE.....	CIPRAYV	CDHDNDCCDG.....	SDEHA.....	C
LRP2_HUMAN	C.....	GGYQFTCPSGR.....	CIYQNWV	CDGEDDCCKDN.....	GDEDG.....	C
LRP2_HUMAN	C.....	SPREWSCPESGR.....	CISYKIV	CDGILDCPGR.....	EDENNTSTGKYC.....	C
LRP2_HUMAN	C.....	GLFSFPCKNGR.....	CVPNYYL	CDGVDDCHDN.....	SDEQL.....	C
LRP2_HUMAN	C.....	SSSAFTCGHGE.....	CIPAHWR	CDKRNDCCVDG.....	SDEHN.....	C
LRP2_HUMAN	C.....	LDTQYTCDNHQ.....	CISKNVV	CDTDNDCCDG.....	SDEKN.....	C
LRP2_HUMAN	C.....	QPSQFNCPNHR.....	CIDLSFV	CDGDKDCVDG.....	SDEVG.....	C
LRP2_HUMAN	C.....	TASQFKCASGDK.....	CIGVTNR	CDGVFDCSDN.....	SDEAG.....	C
LRP2_HUMAN	C.....	HSDEFQCCEDGI.....	CIPNFWE	CDGHPDCLYG.....	SDEHNA.....	C
LRP2_HUMAN	C.....	PSSYFHCDNGN.....	CIHRAWL	CDRDNDCCGM.....	SDEKD.....	C
LRP2_HUMAN	C.....	PSWQWQCLGHNI.....	CVNLSVV	CDGIFDCPNG.....	TDESPL.....	C
LRP2_HUMAN	C.....	GASSFTCSNGR.....	CISEEWK	CDNDNDCCDG.....	SDEMESV.....	C
LRP2_HUMAN	C.....	SPTAFTCANR.....	CVQYSYR	CDYYNDCCDG.....	SDEAG.....	C
LRP2_HUMAN	C.....	NATTEFMCNNRR.....	CIPREFI	CNGVDNCHDNNT.....	SDEKN.....	C
LRP2_HUMAN	C.....	QSGYTKCHNSNI.....	CIPRVYL	CDGDNDCCDN.....	SDENPTY.....	C
LRP2_HUMAN	C.....	SSSEFQCASGR.....	CIPQHWY	CDQETDCFDA.....	SDEPAS.....	C
LRP2_HUMAN	C.....	LADEFKCDGGR.....	CIPSEWI	CDGDNDCCGM.....	SDEKRRHQ.....	C
LRP2_HUMAN	C.....	SDSEFLCVNDRPPDRR.....	CIPQSVV	CDGDVDDCTDG.....	YDENQN.....	C
LRP2_HUMAN	C.....	SENEFTCGYGL.....	CIPKIFR	CDRHNDCCDY.....	SDEGR.....	C
LRP2_HUMAN	C.....	QQNQFTCQNGR.....	CISKTFV	CDENNDCCDG.....	SDELMHL.....	C
LRP2_HUMAN	C.....	PPHEFKCDNGR.....	CIEMMKL	CNHLDDCLDN.....	SDEKG.....	C
LRP2_HUMAN	C.....	SSTQFLCANNEK.....	CIPIWVK	CDGQKDCSDG.....	SDELAL.....	C
LRP2_HUMAN	C.....	RLGQFQCSNGN.....	CTSPQTL	CNAHQNCPDG.....	SDEDRLL.....	C
LRP2_HUMAN	C.....	DSNEWQCANKR.....	CIPESWQ	CDTFNDCCDN.....	SDESSSH.....	C
LRP2_HUMAN	C.....	RPQQFRCANR.....	CIPQAWK	CDVDNDCCGDH.....	SDEPIEE.....	C
LRP2_HUMAN	C.....	DNFTEFSCKTNYR.....	CIPKWAV	CNGVDDCRDN.....	SDEQG.....	C
LRP2_HUMAN	C.....	HPVGDFRCKNHQ.....	CIPLRWQ	CDGQNDCCDN.....	SDEEN.....	C
LRP2_HUMAN	C.....	TESEFRVCNQH.....	CIPSRWI	CDHYNDCCDN.....	SDERD.....	C
LRP2_HUMAN	C.....	HPEYFQCTSGH.....	CVHSELK	CDGSADCLDA.....	SDEAD.....	C
LRP2_HUMAN	C.....	QATMFECCKNHV.....	CIPPYWK	CDGDDDCGDG.....	SDEELHL.....	C
LRP2_HUMAN	C.....	NSPNRFRCDNNR.....	CIYSHEV	CNGVDDCCDG.....	TDETEEH.....	C
LRP2_HUMAN	C.....	TEYEEKCGNGH.....	CIPHDNV	CDDADDCGDW.....	SDELG.....	C
LR1B_HUMAN	C.....	DPGEFLCHDHVT.....	CVSQSWL	CDGDPDCPDD.....	SDESOLDT.....	C

LR1B_HUMAN	C.....	PLNHIACLGTNK.....	CVHLSQL.CNGVLDCPDG.....	YDEGVH.....	C
LR1B_HUMAN	C.....	KAGEFRCKNRH.....	CIQARWK.CDGDDDCLDG.....	SDEDSVN.....	C
LR1B_HUMAN	C.....	PDDQFKCQNNR.....	CIPKRWL.CDGANDCGSN.....	EDESNOT.....	C
LR1B_HUMAN	C.....	QVDQFSCGNGR.....	CIPRAWL.CDREDDCGDQ.....	TDEMAS.....	C
LR1B_HUMAN	C.....	EPLTQFVCKSGR.....	CISSEWH.CDSDDDCGDG.....	SDEVG.....	C
LR1B_HUMAN	C.....	FDNQFRCSSGR.....	CIPGHWL.CDGDNDGDF.....	SDEAQIN.....	C
LR1B_HUMAN	C.....	NGNEFQCHPDGN.....	CVPDLWR.CDGEKDCEDG.....	SDEKG.....	C
LR1B_HUMAN	C.....	DHKTKFSCWSTGR.....	CINKAWV.CDGDIDCEDQ.....	SDEDD.....	C
LR1B_HUMAN	C.....	GPPKHPCANDTSV.....	CLQPEKL.CNGKKDCPDG.....	SDEGYL.....	C
LR1B_HUMAN	C.....	NAYSEFECNGE.....	CIDYQLT.CDGIPHCKDK.....	SDEKLLY.....	C
LR1B_HUMAN	C.....	RRGFKPCYNRR.....	CIPHGKL.CDGENDCGDN.....	SDELD.....	C
LR1B_HUMAN	C.....	ATVEFRCADGT.....	CIPRSAR.CNQNICADA.....	SDEKN.....	C
LR1B_HUMAN	C.....	CTHFYKLGVKTTGFIRCNSTSL.....	CVLPTWI.CDGSNDGCGDY.....	SDELK.....	C
LR1B_HUMAN	C.....	EENYFSCPSGR.....	CILNTWI.CDGQKDCEDG.....	RDEFH.....	C
LR1B_HUMAN	C.....	SWNQFACSAQK.....	CISKHWI.CDGEDDCGDG.....	LDESISI.....	C
LR1B_HUMAN	C.....	AADMFSCQGSRA.....	CVPRHWL.CDGERDCPDG.....	SDELSTAG.....	C
LR1B_HUMAN	C.....	DENAFMCHNKV.....	CIPKQFV.CDHDDDCGDG.....	SDESPQ.....	C
LR1B_HUMAN	C.....	GTEEFSCADGR.....	CLLNTQWQCDGDFDCPDH.....	SDEAPLNPK.....	C
LR1B_HUMAN	C.....	NSSFFMCKNGR.....	CIPSGGL.CDNKDDCGDG.....	SDEAN.....	C
LR1B_HUMAN	C.....	TASQFRCKTDK.....	CIPFWWK.CDTVDDCGDG.....	SDEPDD.....	C
LR1B_HUMAN	C.....	QPGRFQCGTGL.....	CALPAFI.CDGENDCGDN.....	SDELN.....	C
LR1B_HUMAN	C.....	LSGQFKCTKNQK.....	CIPVNLN.CNGQDDCGDE.....	EDERD.....	C
LR1B_HUMAN	C.....	SPDYFQCKTTKH.....	CISKLWV.CDEDPCADA.....	SDEAN.....	C
LR1B_HUMAN	C.....	GPHEFQCKNNN.....	CIPDHWR.CDSQNDGSDN.....	SDEEN.....	C
LR1B_HUMAN	C.....	TLKDFLCANGD.....	CVSSRFW.CDGFDFCADG.....	SDEAN.....	C
LR1B_HUMAN	C.....	SKDQFRCNNGQ.....	CIPAKWK.CDGHEDECKYG.....	EDEKS.....	C
LR1B_HUMAN	C.....	SSREYICASDG.....	CISASLK.CNGEYDCADG.....	SDEMD.....	C
LR1B_HUMAN	C.....	KEDQFRCKNAH.....	CIPIRWL.CDGIHDCVDG.....	SDEEN.....	C
LR1B_HUMAN	C.....	RADEFLCNNSL.....	CKLHFVW.CDGEDDCGDN.....	SDEAPDM.....	C
LR1B_HUMAN	C.....	PSTRPHRCRNNRI.....	CLQSEQM.CNGIDECGDN.....	SDEDH.....	C
LR1B_HUMAN	C.....	KKDEFACSNKK.....	CIPMDLQ.CDRLDDCGDG.....	SDEQG.....	C

075851	C.....	AEGEALCQENGH.....	CVPHGWL.CDNQDDCGDG.....	SDEEGE.....	C
075851	C.....	GEGQMTCSSEH.....	CLPLALL.CDRQDDCGDG.....	TDEPSYP.....	C
075851	C.....	PQGLLACADGR.....	CLPPALL.CDGHPCDLDA.....	ADEES.....	C
075851	C.....	VPGEVSCVDGT.....	CLGAIQL.CDGVWDCPDG.....	ADEGPGH.....	C

ENSP00000262089

= 075851	C.....	GPFEFRCSGE.....	CTPRGWR.CDQEEDCADG.....	SDERG.....	C
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ENSP00000262089

075851	C.....	APHHAPCARGPH.....	CVSPEQL.CDGVRQCPDG.....	SDEGPDA.....	C
075851	C.....	PGLFPCGVAPGL.....	CLTPEQL.CDGIPDCPDG.....	EDELN.....	C
075851	C.....	PEYTCPNGT.....	CIGFQLV.CDGQPDGPRGQVGPSPEEQ.....	SDEEQ.....	C
075851	C.....	EPGVGLRCASGE.....	CVLRGGP.CDGVLDCEDEG.....	SDEEG.....	C

ENSP00000262089

075851	C.....	GPGQTPCEVLG.....	CVEQAQV.CDGREDCLDG.....	SDERH.....	C
075851	C.....	SPSQLSCSGE.....	CLSAERR.CDLRPDCQDG.....	SDEEG.....	C
C18ORF1	C.....	KFTCTSGK.....	CLYLGLSLVCNQNDGDN.....	SDEEN.....	C

AAH07083/Q9NPF0

AAH07083/Q9NPF0	C.....	PPTKFQCRTSGL.....	CVPLTWR.CDRDLDCSDG.....	SDEEE.....	C
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AAH07083/Q9NPF0

Q9HBX9	C.....	LAGELRCTLSDD.....	CIPLTWR.CDGHPCDPS.....	SDELG.....	C
Q9BY79/Q96DQ9	C.....	SLGYFPCGNITK.....	CLPQLLH.CNGVDDCGNQ.....	AEDN.....	C
Q9BY79/Q96DQ9	C.....	AHDEFRCQDLI.....	CLLPDSV.CDGFANCADG.....	SDET.....	C
Q9BY79/Q96DQ9	C.....	GPSELSCQAGG.....	CKGVQWM.CDMWRDCTDG.....	SDDN.....	C

BAB55257 =

ENSP00000239367

095518 =	C.....	SRYHFFCDDGC.....	CIDITLA.CDGVQCPDG.....	SDEDF.....	C	
ENSP00000255793	C.....	PGEFLCSVNGL.....	CVPA.....	CDGVKDCPNG.....	LDERN.....	C

ENSP00000255793

ENSP00000255793	C.....	RATFQCKEDST.....	CISLPKV.CDGQPDCLNG.....	SDEEQ.....	C
-----------------	--------	------------------	-------------------------	------------	---

ENSP00000255793

ENSP00000255793	C.....	GTFTFQCEDRS.....	CVKKPNPQCDGRPDG.....	SDEEH.....	C
-----------------	--------	------------------	----------------------	------------	---

ENSP00000255793

Q8WXD0	C	QKGYFPCGNLTK	CLPRAFH	CDGKDDCGNG	ADEEN	C
Q8NB0	C	STARYHCKNGL	CIDKSF	CDGQNNCQDN	SDEES	C
Q8NB0	C	GPTFFPCASGIH	CIIGRFR	CNGFEDCPDG	SDEEN	C
Q8NB0	C	NIPGNFMCSNGR	CIPGAWQ	CDGLPDCFDK	SDEKE	C
MEGF7	C	ALDQFLCWNGR	CIGQRKL	CNGVNDGCGN	SDESPQON	C
MEGF7	C	EEDEFPCQNGY	CIRSLWH	CDGDNDGCGN	SDEQ	C
MEGF7	C	RSGEFMCDSGL	CINAGWR	CDGDADCDQ	SDEEN	C
MEGF7	C	TAEQFRCHSGR	CVRLSWR	CDGEDDCADN	SDEEN	C
MEGF7	C	SPLDFHCDNGK	CIRRSWV	CDGDNDGCGN	SDEQ	C
MEGF7	C	NLEEFQCAAGR	CILDIYH	CDGDDDCGDW	SDESD	C
MEGF7	C	SDKEFRCSGDS	CIAEHVY	CDGDTDCCKDG	SDEEN	C

MEGF7	C	GRSHFTCAVSALGE <u>C</u> T	CIPAQQWQ	CDGDNDGCDH	SDEDG	C
CAD61944	C	LQEEFQCLNHR	CVSAVQR	CDGVDACGDG	SDEAG	C
CAD61944	C	PPGHFPCGAAGTSGATA	CYLPADR	CNYQTFCADG	ADERR	C
CAD61944	C	QPGNFRCRDEK	CVYETWV	CDGQPDGADG	SDEWD	C
ENSG00000181006						
	C	PEITDFLCRDKK	CIASHLL	CDYKPDGSDR	SDEAH	C
ENSP00000320248						
	C	NNRTFKCGNDI	CFRKQNAKCDGTVDCPDG		SDEEG	C
ENSP00000277547						
	C	PPGHHHCQNKV	CVEPQQL	CDGEDNCGDL	SDENPLT	C
ENSP00000320022						
	C	KQGHLAGDL	CVPPEQL	CDFEEQCAGG	EDEQA	C
ENSP00000313222						
	C	PGNSFSCGNSQ	CVTKVNPECDDQEDCSDG		SDEAH	C

Figure 11

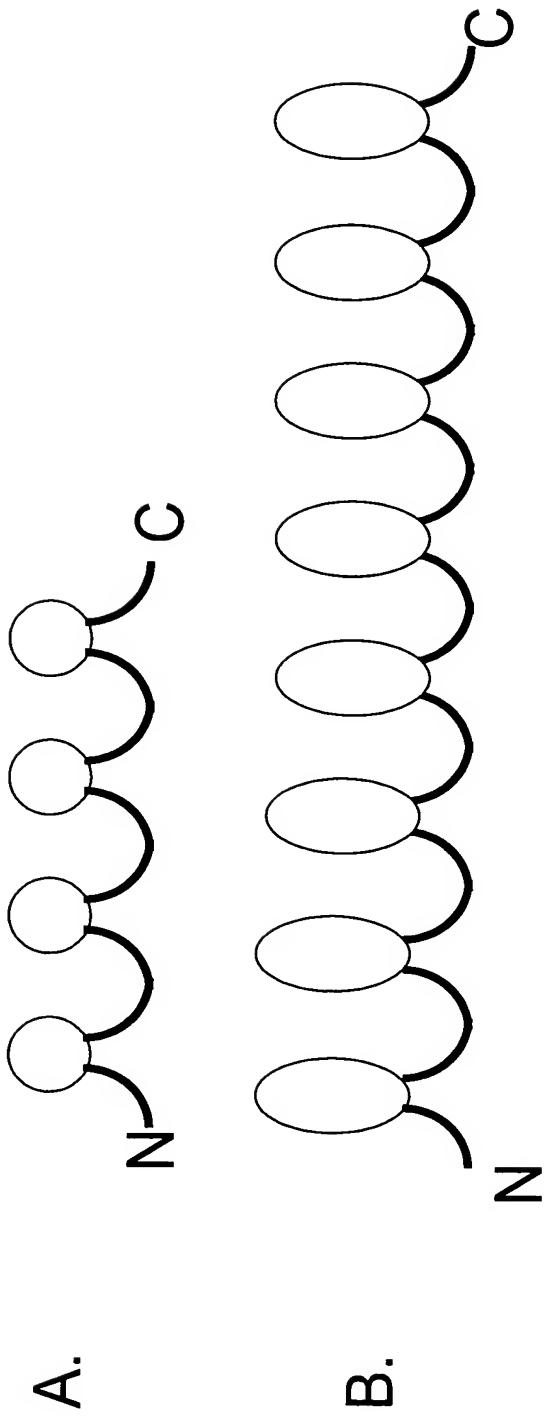
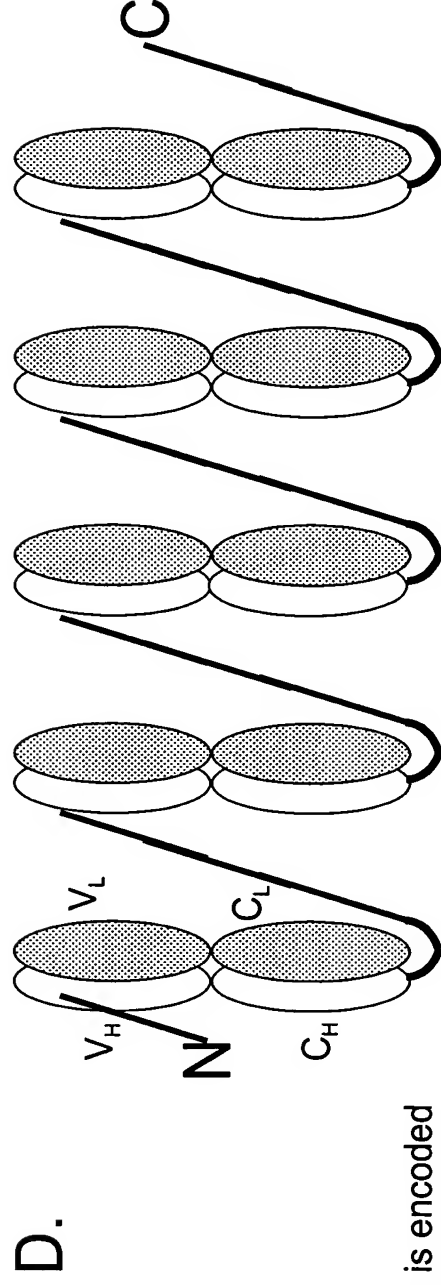
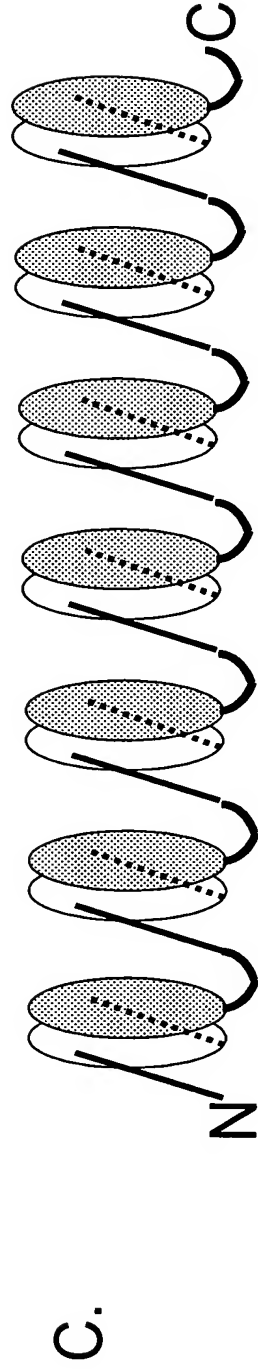


Figure 11



Light chain is encoded
as a separate protein

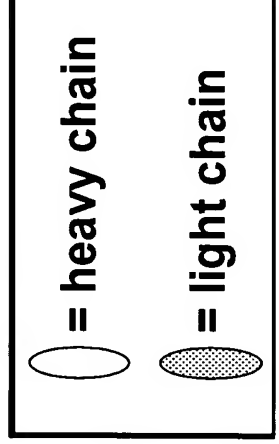
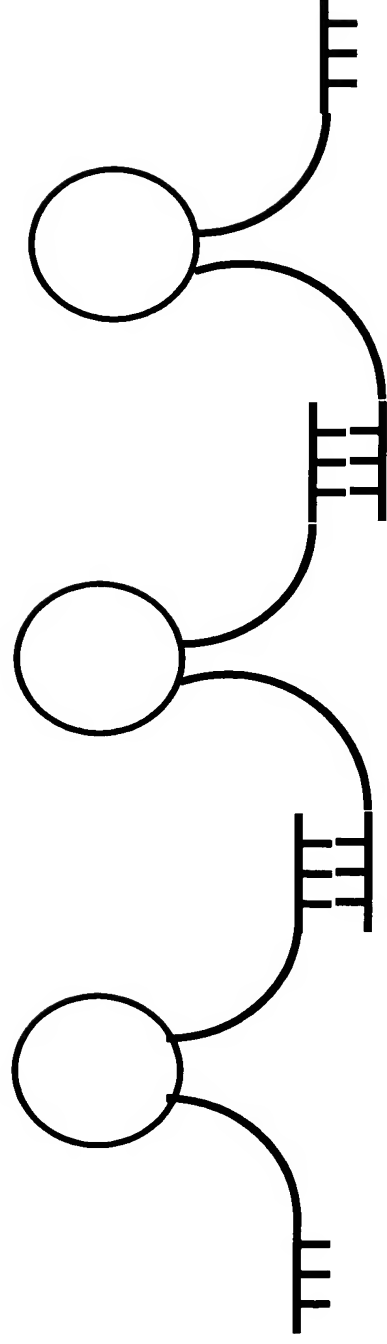


Figure 12

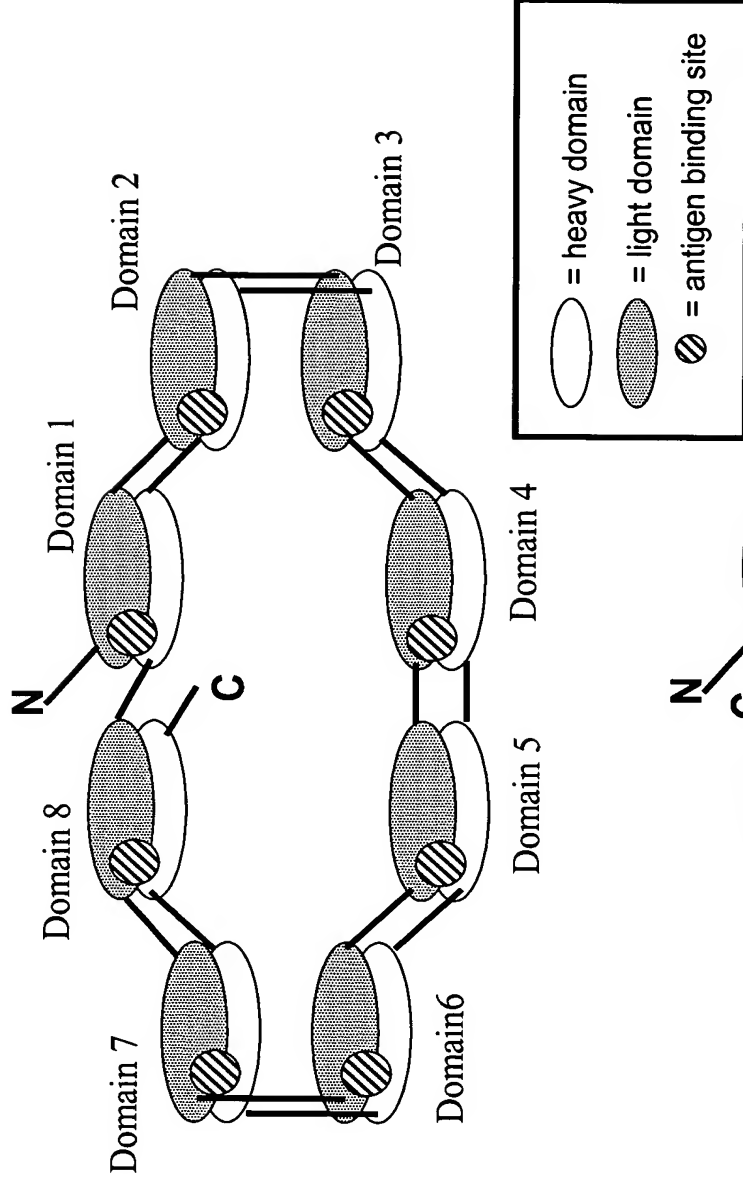


○ = any monomer domain
▮ = obligate heterodimeric linker

Figure 13

A.

One Chain
Multimer of
Fv's



B.

Two Chain
Multimer of
Fv's

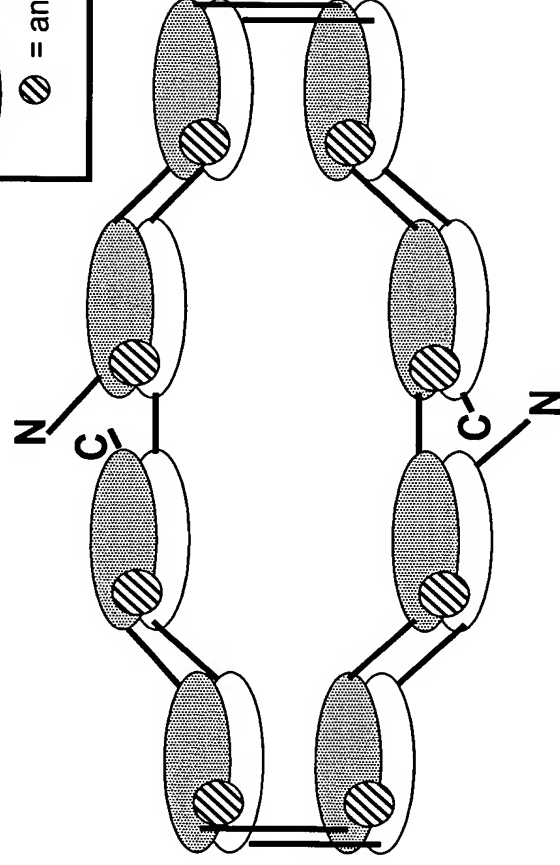


Figure 13C

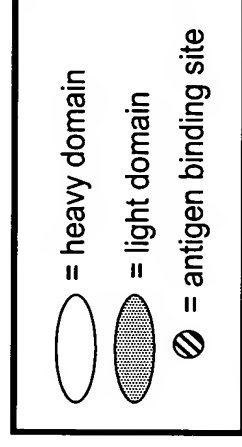
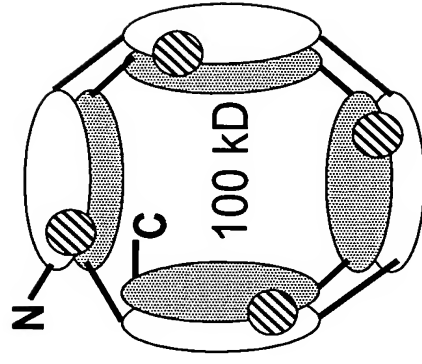


Figure 14

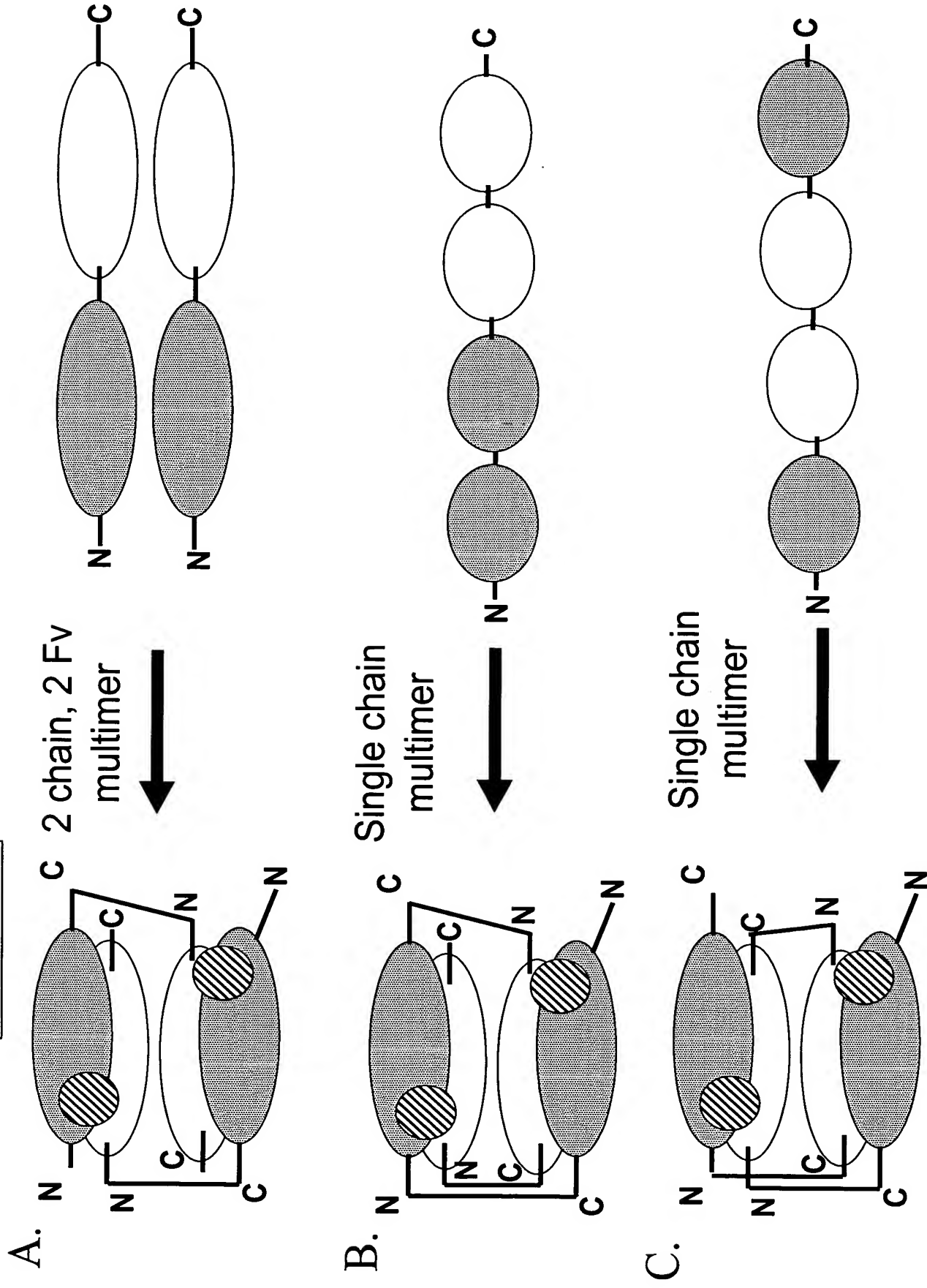


Figure 15

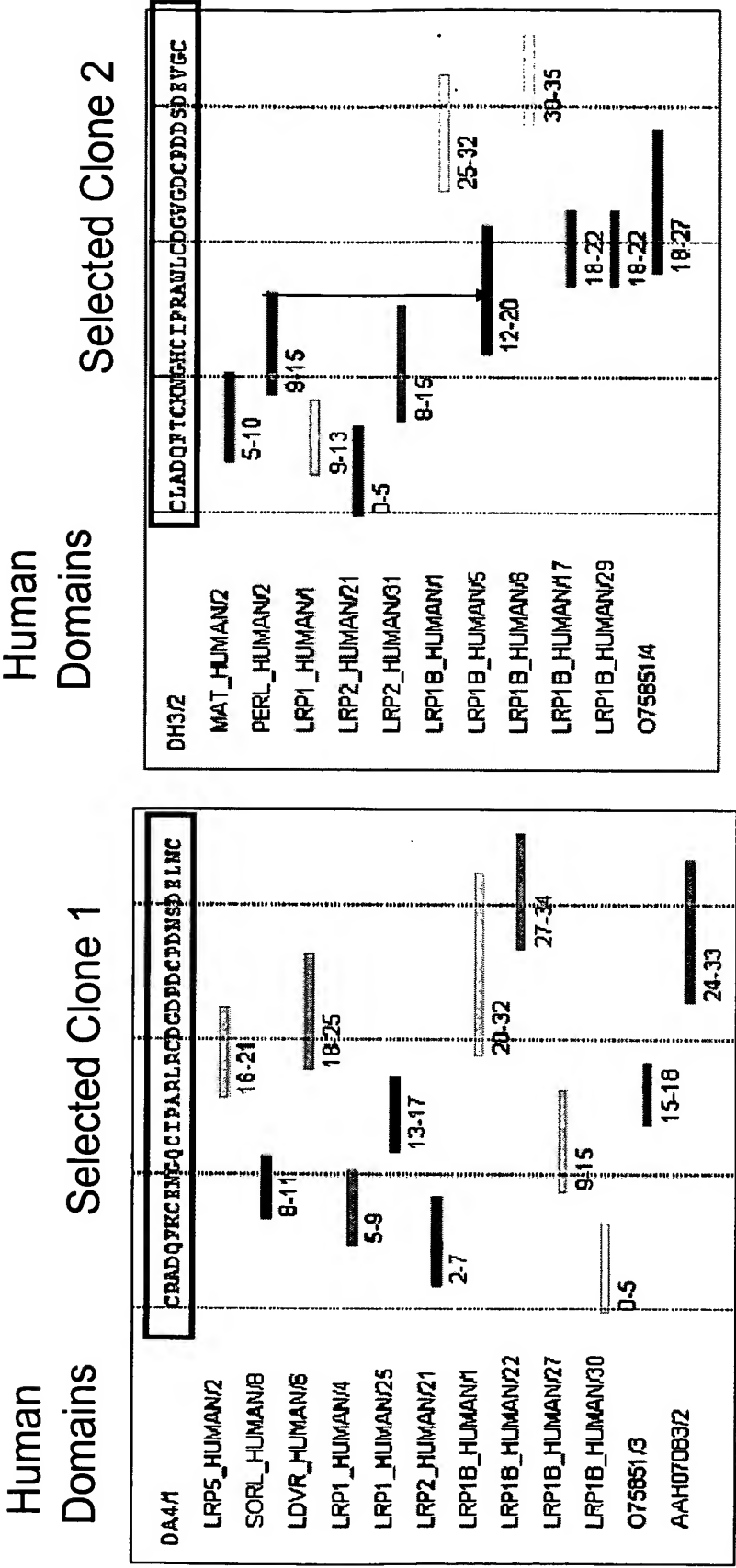


Figure 16
Cell Killing induced by Maxybodies

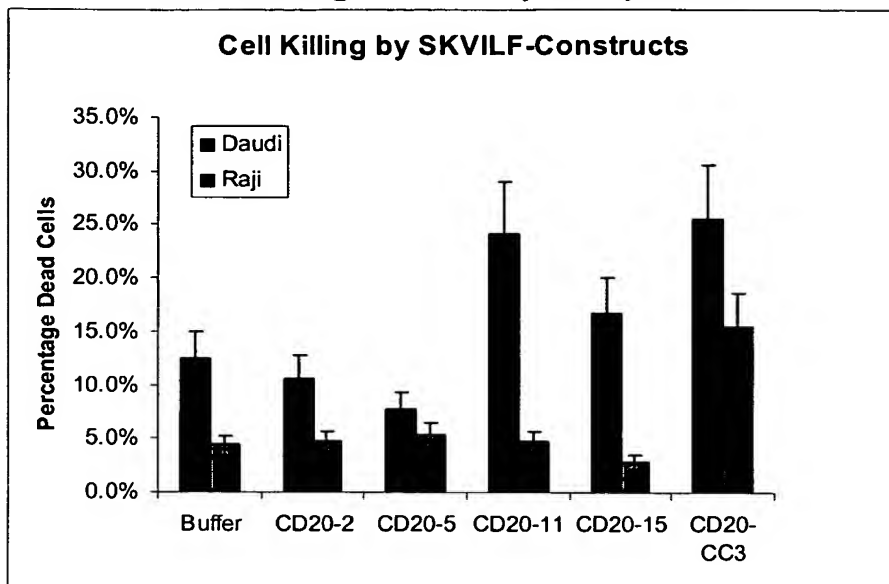


Figure 17: TPO-R Phage Specificity Data

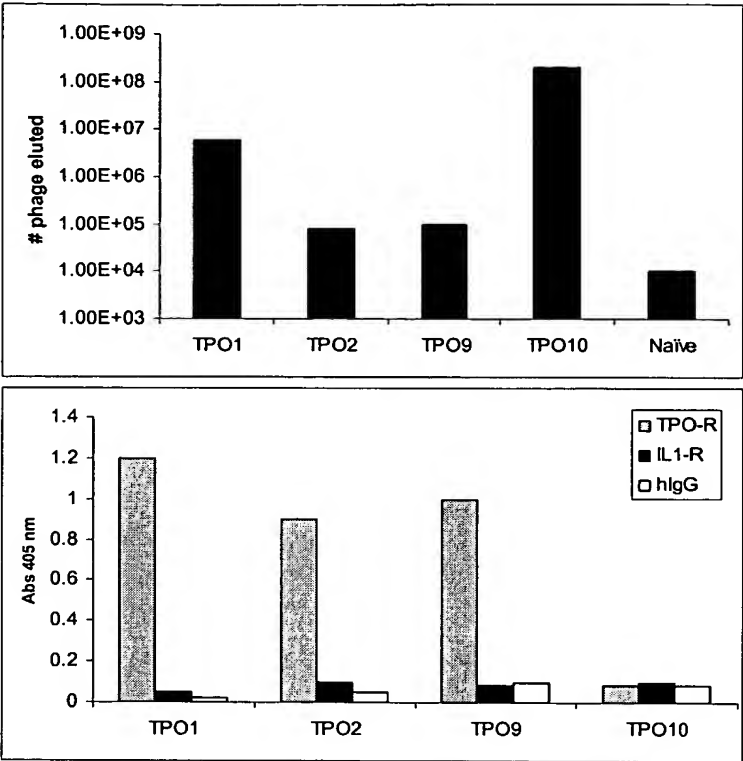


Figure 18: TF1 Proliferation Assay

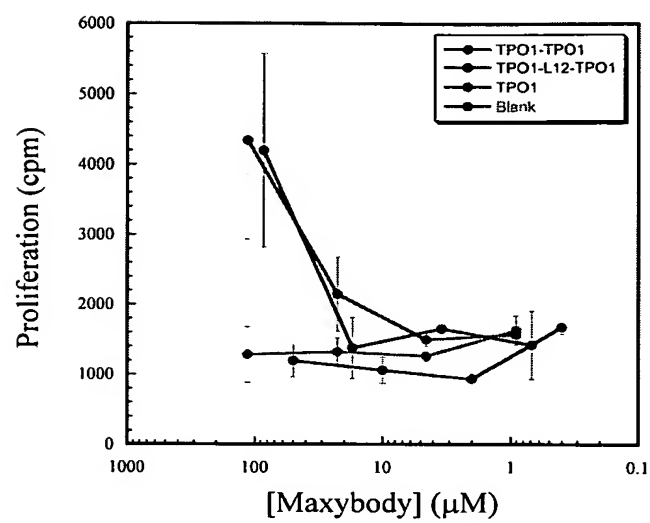


Figure 19 : Epitope mapping of IgE-Binding Monomer

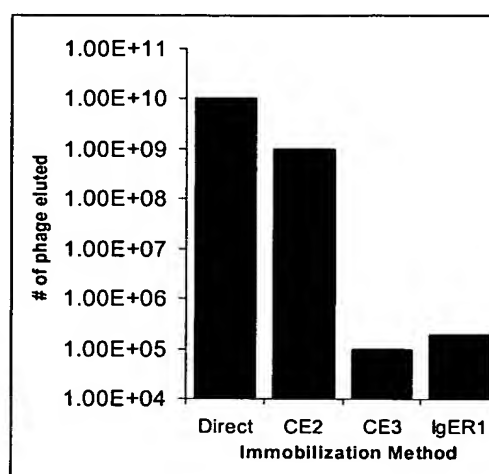


Figure 20

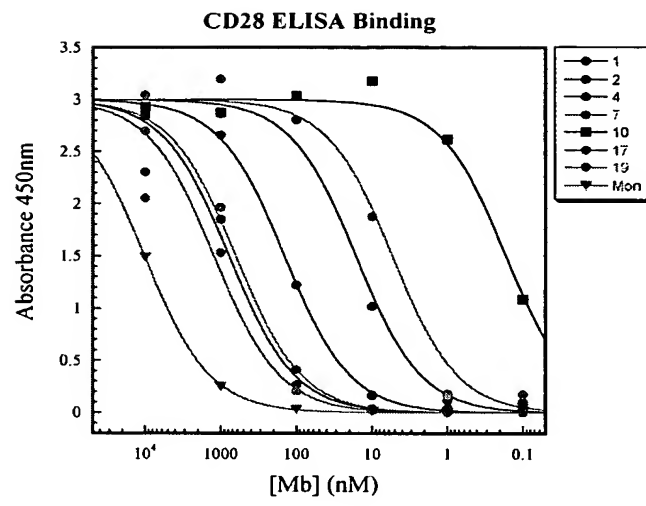


Figure 21

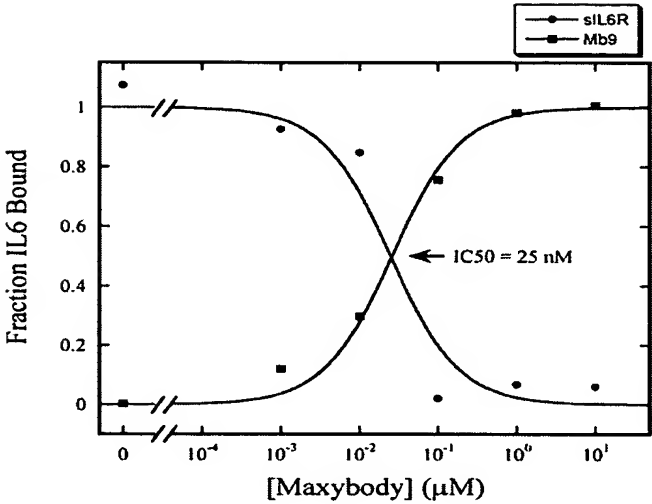


Figure 22

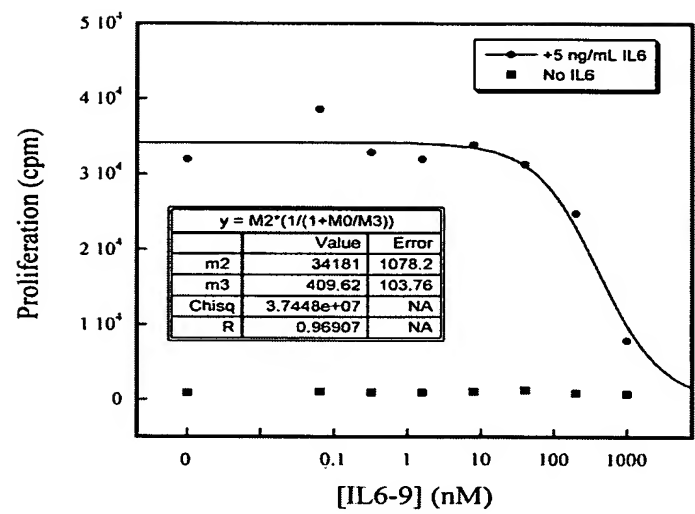


Figure 23

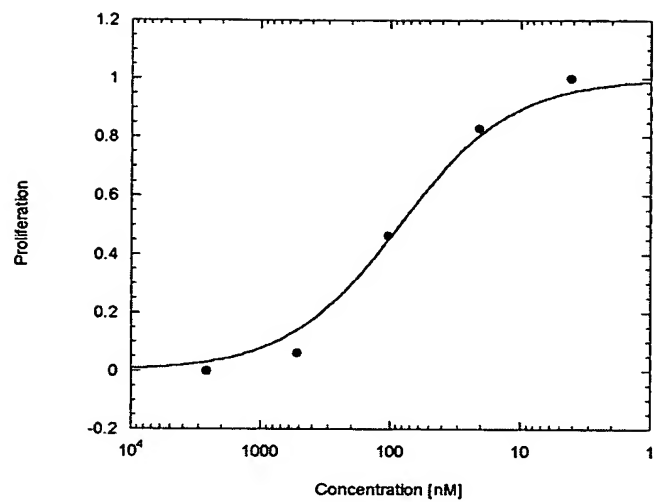


Figure 24

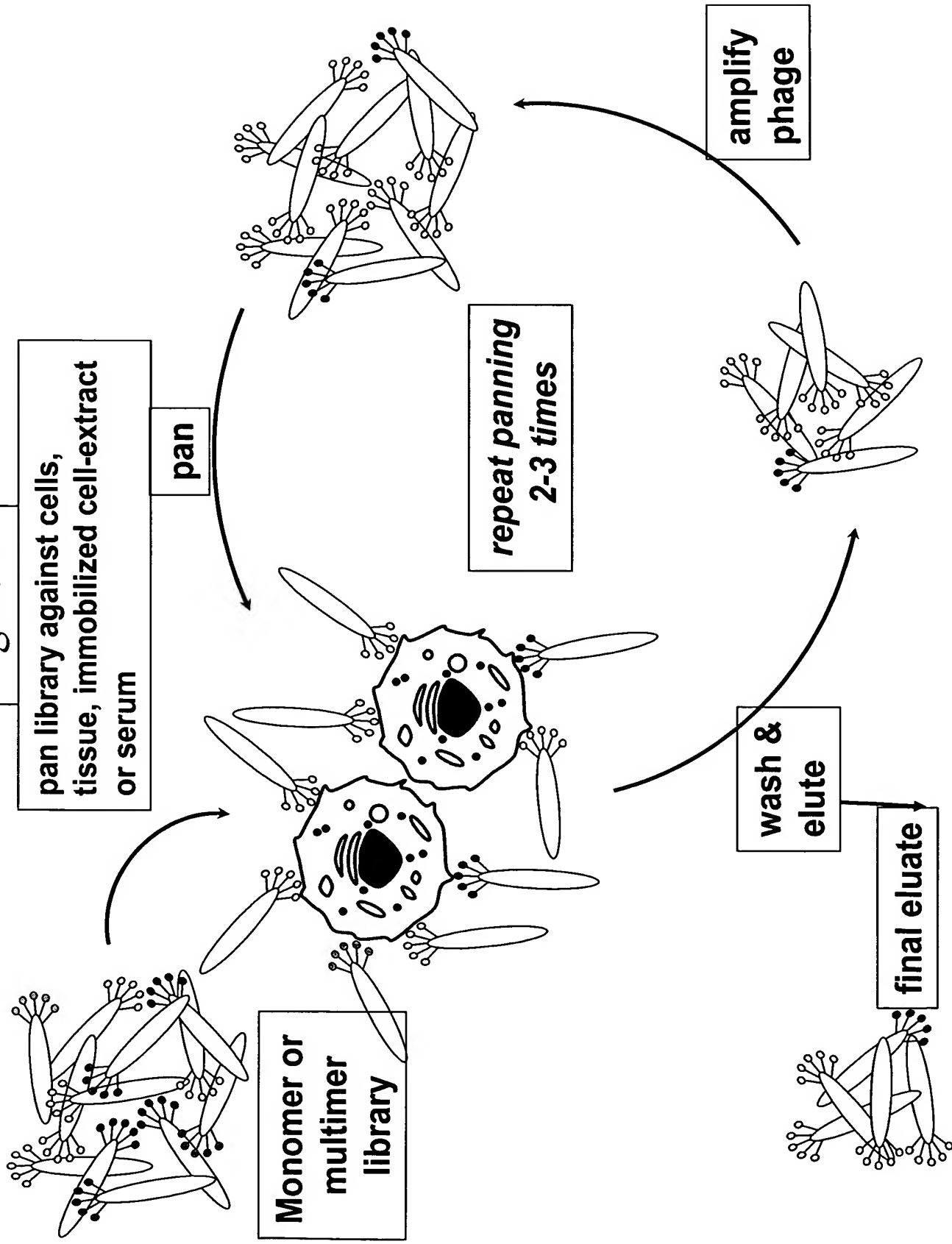


Figure 25

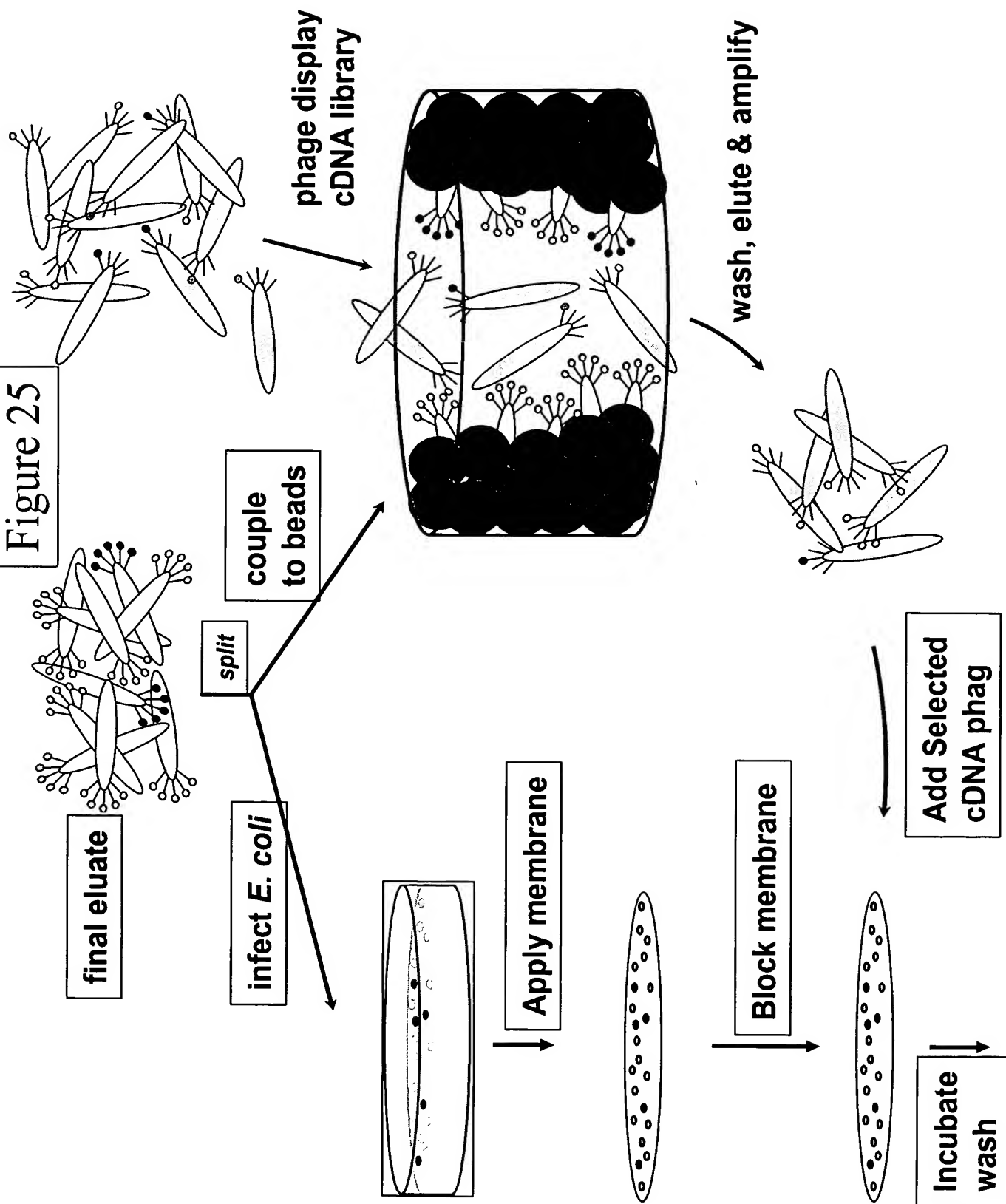
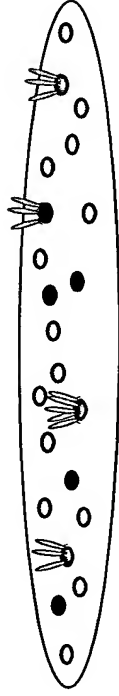
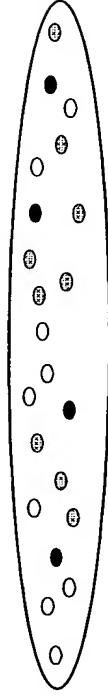


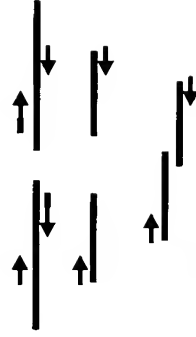
Figure 26



Stain membrane using cDNA phage specific MAb (HRP labeled)
Add substrate



Cut positive spots out of membrane and add to PCR tube
PCR amplify cDNA and MB sequences



Sequence PCR fragments

Figure 27

Format Variations

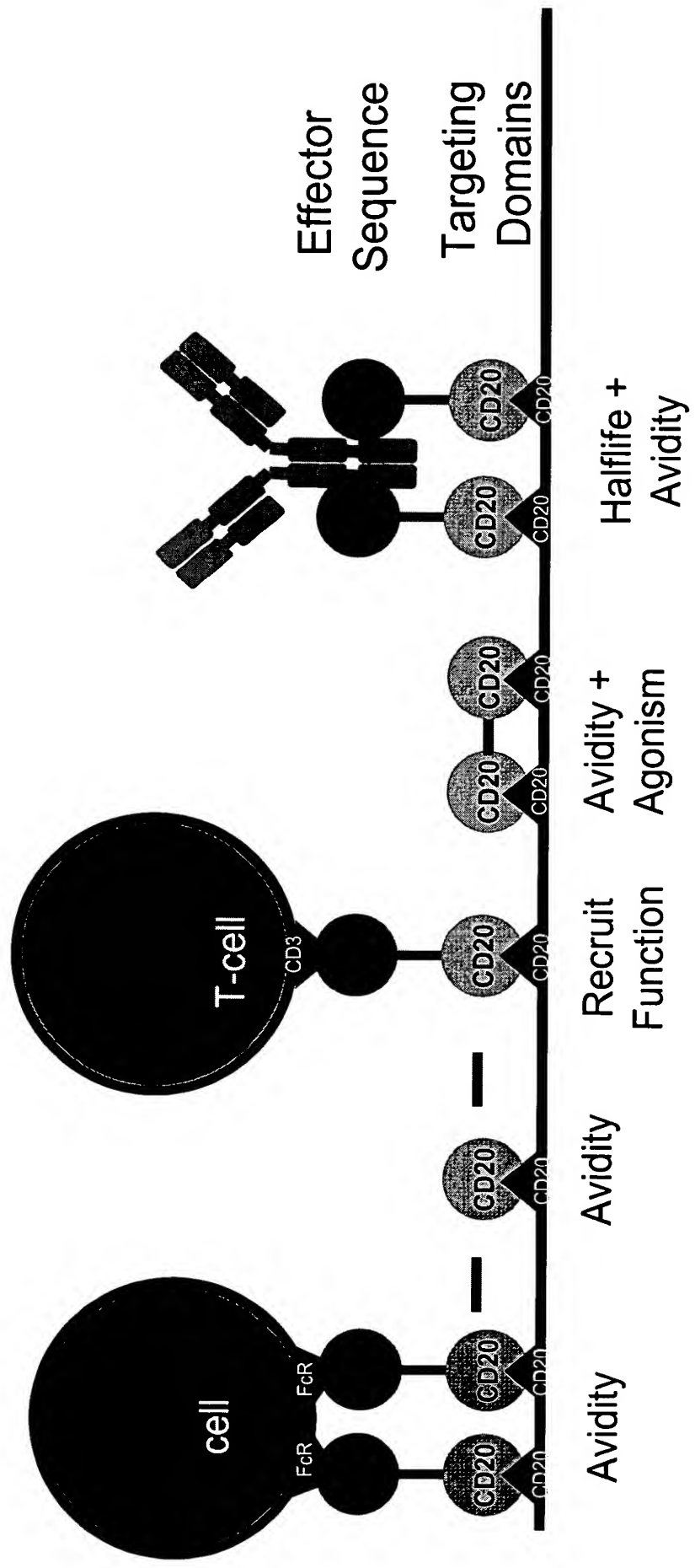
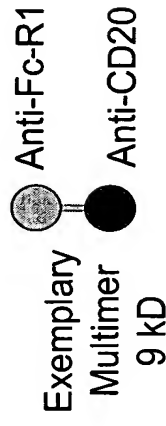


Figure 28

Multimer Format



Monovalent Binding

Complex Stabilization

